PCT1

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RAW SEQUENCE LISTING DATE: 08/14/2002
PATENT APPLICATION: **US/10/019,816** TIME: 09:38:12

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\08142002\J019816.raw**

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      3 <110> APPLICANT: AGREZ, MICHAEL V
      4       AHMED, NUZHAT
      6 <120> TITLE OF INVENTION: A METHOD OF MODULATING INTEGRIN MEDIATED CELLULAR ACTIVITY
AND AGENTS
      7       USEFUL FOR SAME
      9 <130> FILE REFERENCE: SW-046 XX
     11 <140> CURRENT APPLICATION NUMBER: US 10/019,816
     12 <141> CURRENT FILING DATE: 2000-06-28
     14 <150> PRIOR APPLICATION NUMBER: PQ 1248
     15 <151> PRIOR FILING DATE: 1999-06-28
     17 <150> PRIOR APPLICATION NUMBER: PQ 8003
     18 <151> PRIOR FILING DATE: 2000-06-06
     20 <160> NUMBER OF SEQ ID NOS: 23
     22 <170> SOFTWARE: PatentIn version 3.1
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 788
     26 <212> TYPE: PRT
     27 <213> ORGANISM: HOMO SAPIENS
     29 <400> SEQUENCE: 1
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     32 1               5                  10                  15
     35 Asp Ser Arg Thr Arg Trp Leu Cys Leu Gly Gly Ala Glu Thr Cys Glu
     36             20                  25                  30
     39 Asp Cys Leu Leu Ile Gly Pro Gln Cys Ala Trp Cys Ala Gln Glu Asn
     40         35                  40                  45
     43 Phe Thr His Pro Ser Gly Val Gly Glu Arg Cys Asp Thr Pro Ala Asn
     44     50                  55                  60
     47 Leu Leu Ala Lys Gly Cys Gln Leu Asn Phe Ile Glu Asn Pro Val Ser
     48 65                  70                  75                  80
     51 Gln Val Glu Ile Leu Lys Asn Lys Pro Leu Ser Val Gly Arg Gln Lys
     52                 85                  90                  95
     55 Asn Ser Ser Asp Ile Val Gln Ile Ala Pro Gln Ser Leu Ile Leu Lys
     56             100                 105                 110
     59 Leu Arg Pro Gly Gly Ala Gln Thr Leu Gln Val His Val Arg Gln Thr
     60         115                 120                 125
     63 Glu Asp Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu Ser Ala Ser
     64     130                 135                 140
     67 Met Asp Asp Asp Leu Asn Thr Ile Lys Glu Leu Gly Ser Gly Leu Ser
     68 145                 150                 155                 160
     71 Lys Glu Met Ser Lys Leu Thr Ser Asn Phe Arg Leu Gly Phe Gly Ser
     72                 165                 170                 175
     75 Phe Val Glu Lys Pro Val Ser Pro Phe Val Lys Thr Thr Pro Glu Glu
     76             180                 185                 190
     79 Ile Ala Asn Pro Cys Ser Ser Ile Pro Tyr Phe Cys Leu Pro Thr Phe
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80          195                 200                 205
83 Gly Phe Lys His Ile Leu Pro Leu Thr Asn Asp Ala Glu Arg Phe Asn
84      210                 215                 220
87 Glu Ile Val Lys Asn Gln Lys Ile Ser Ala Asn Ile Asp Thr Pro Glu
88 225                 230                 235                 240
91 Gly Gly Phe Asp Ala Ile Met Gln Ala Ala Val Cys Lys Glu Lys Ile
92                  245                 250                 255
95 Gly Trp Arg Asn Asp Ser Leu His Leu Leu Val Phe Val Ser Asp Ala
96              260                 265                 270
99 Asp Ser His Phe Gly Met Asp Ser Lys Leu Ala Gly Ile Val Ile Pro
100         275                 280                 285
103 Asn Asp Gly Leu Cys His Leu Asp Ser Lys Asn Glu Tyr Ser Met Ser
104     290                 295                 300
107 Thr Val Leu Glu Tyr Pro Thr Ile Gly Gln Leu Ile Asp Lys Leu Val
108 305                 310                 315                 320
111 Gln Asn Asn Val Leu Leu Ile Phe Ala Val Thr Gln Glu Gln Val His
112                 325                 330                 335
115 Leu Tyr Glu Asn Tyr Ala Lys Leu Ile Pro Gly Ala Thr Val Gly Leu
116             340                 345                 350
119 Leu Gln Lys Asp Ser Gly Asn Ile Leu Gln Leu Ile Ile Ser Ala Tyr
120         355                 360                 365
123 Glu Glu Leu Arg Ser Glu Val Glu Leu Glu Val Leu Gly Asp Thr Glu
124     370                 375                 380
127 Gly Leu Asn Leu Ser Phe Thr Ala Ile Cys Asn Asn Gly Thr Leu Phe
128 385                 390                 395                 400
131 Gln His Gln Lys Lys Cys Ser His Met Lys Val Gly Asp Thr Ala Ser
132                 405                 410                 415
135 Phe Ser Val Thr Val Asn Ile Pro His Cys Glu Arg Arg Ser Arg His
136             420                 425                 430
139 Ile Ile Ile Lys Pro Val Gly Leu Gly Asp Ala Leu Glu Leu Leu Val
140         435                 440                 445
143 Ser Pro Glu Cys Asn Cys Asp Cys Gln Lys Glu Val Glu Val Asn Ser
144     450                 455                 460
147 Ser Lys Cys His His Gly Asn Gly Ser Phe Gln Cys Gly Val Cys Ala
148 465                 470                 475                 480
151 Cys His Pro Gly His Met Gly Pro Arg Cys Glu Cys Gly Glu Asp Met
152                 485                 490                 495
155 Leu Ser Thr Asp Ser Cys Lys Glu Ala Pro Asp His Pro Ser Cys Ser
156             500                 505                 510
159 Gly Arg Gly Asp Cys Tyr Cys Gly Gln Cys Ile Cys His Leu Ser Pro
160         515                 520                 525
163 Tyr Gly Asn Ile Tyr Gly Pro Tyr Cys Gln Cys Asp Asn Phe Ser Cys
164     530                 535                 540
167 Val Arg His Lys Gly Leu Leu Cys Gly Gly Asn Gly Asp Cys Asp Cys
168 545                 550                 555                 560
171 Gly Glu Cys Val Cys Arg Ser Gly Trp Thr Gly Glu Tyr Cys Asn Cys
172                 565                 570                 575
175 Thr Thr Ser Thr Asp Ser Cys Val Ser Glu Asp Gly Val Leu Cys Ser
176             580                 585                 590
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179 Gly Arg Gly Asp Cys Val Cys Gly Lys Cys Val Cys Thr Asn Pro Gly
180         595                 600                 605
183 Ala Ser Gly Pro Thr Cys Glu Arg Cys Pro Thr Cys Gly Asp Pro Cys
184     610                 615                 620
187 Asn Ser Lys Arg Ser Cys Ile Glu Cys His Leu Ser Ala Ala Gly Gln
188 625                 630                 635                 640
191 Ala Gly Glu Glu Cys Val Asp Lys Cys Lys Leu Ala Gly Ala Thr Ile
192                 645                 650                 655
195 Ser Glu Glu Glu Asp Phe Ser Lys Asp Gly Ser Val Ser Cys Ser Leu
196             660                 665                 670
199 Gln Gly Glu Asn Glu Cys Leu Ile Thr Phe Leu Ile Thr Thr Asp Asn
200         675                 680                 685
203 Glu Gly Lys Thr Ile Ile His Ser Ile Asn Glu Lys Asp Cys Pro Lys
204     690                 695                 700
207 Pro Pro Asn Ile Pro Met Ile Met Leu Gly Val Ser Leu Ala Thr Leu
208 705                 710                 715                 720
211 Leu Ile Gly Val Val Leu Leu Cys Ile Trp Lys Leu Leu Val Ser Phe
212                 725                 730                 735
215 His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
216             740                 745                 750
219 Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
220         755                 760                 765
223 Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
224     770                 775                 780
227 Ser Thr Asp Cys
228 785
231 <210> SEQ ID NO: 2
232 <211> LENGTH: 15
233 <212> TYPE: PRT
234 <213> ORGANISM: HOMO SAPIENS
236 <400> SEQUENCE: 2
238 Arg Ser Lys Ala Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg
239 1               5                   10                  15
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 10
244 <212> TYPE: PRT
245 <213> ORGANISM: HOMO SAPIENS
247 <400> SEQUENCE: 3
249 Arg Ser Lys Ala Lys Asn Pro Leu Tyr Arg
250 1               5                   10
253 <210> SEQ ID NO: 4
254 <211> LENGTH: 5
255 <212> TYPE: PRT
256 <213> ORGANISM: HOMO SAPIENS
258 <400> SEQUENCE: 4
260 Arg Ser Lys Ala Lys
261 1               5
264 <210> SEQ ID NO: 5
265 <211> LENGTH: 5
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266 <212> TYPE: PRT
267 <213> ORGANISM: HOMO SAPIENS
269 <400> SEQUENCE: 5
271 Asn Pro Leu Tyr Arg
272 1               5
275 <210> SEQ ID NO: 6
276 <211> LENGTH: 41
277 <212> TYPE: PRT
278 <213> ORGANISM: HOMO SAPIENS
280 <400> SEQUENCE: 6
282 His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala
283 1               5                   10                  15
286 Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr
287             20                  25                  30
290 Val Val Asn Pro Lys Tyr Glu Gly Lys
291         35                  40
294 <210> SEQ ID NO: 7
295 <211> LENGTH: 40
296 <212> TYPE: PRT
297 <213> ORGANISM: HOMO SAPIENS
299 <400> SEQUENCE: 7
301 Ser Asp Leu Arg Glu Tyr Arg Arg Phe Glu Lys Glu Lys Leu Lys Ser
302 1               5                   10                  15
305 Gln Trp Asn Asn Asp Asn Pro Leu Phe Lys Ser Ala Thr Thr Thr Val
306             20                  25                  30
309 Met Asn Pro Lys Phe Ala Glu Ser
310         35                  40
313 <210> SEQ ID NO: 8
314 <211> LENGTH: 41
315 <212> TYPE: PRT
316 <213> ORGANISM: HOMO SAPIENS
318 <400> SEQUENCE: 8
320 His Asp Arg Lys Glu Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg Ala
321 1               5                   10                  15
324 Lys Trp Asp Thr Ala Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr
325             20                  25                  30
328 Phe Thr Asn Ile Thr Tyr Arg Gly Thr
329         35                  40
332 <210> SEQ ID NO: 9
333 <211> LENGTH: 52
334 <212> TYPE: PRT
335 <213> ORGANISM: HOMO SAPIENS
337 <400> SEQUENCE: 9
339 His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
340 1               5                   10                  15
343 Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
344             20                  25                  30
347 Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
348         35                  40                  45
```

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351 Ser Thr Asp Ser
352     50
355 <210> SEQ ID NO: 10
356 <211> LENGTH: 52
357 <212> TYPE: PRT
358 <213> ORGANISM: HOMO SAPIENS
360 <400> SEQUENCE: 10
362 His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
363 1               5                  10                  15
366 Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
367             20                  25                  30
370 Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
371         35                  40                  45
374 Ser Thr Asp Cys
375     50
378 <210> SEQ ID NO: 11
379 <211> LENGTH: 22
380 <212> TYPE: PRT
381 <213> ORGANISM: HOMO SAPIENS
383 <400> SEQUENCE: 11
385 His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
386 1               5                  10                  15
389 Lys Trp Gln Thr Gly Thr
390             20
393 <210> SEQ ID NO: 12
394 <211> LENGTH: 20
395 <212> TYPE: PRT
396 <213> ORGANISM: HOMO SAPIENS
398 <400> SEQUENCE: 12
400 Arg Ser Lys Ala Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly
401 1               5                  10                  15
404 Ser Thr Ser Thr
405             20
408 <210> SEQ ID NO: 13
409 <211> LENGTH: 20
410 <212> TYPE: PRT
411 <213> ORGANISM: HOMO SAPIENS
413 <400> SEQUENCE: 13
415 Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr Phe Lys Asn Val Thr Tyr
416 1               5                  10                  15
419 Lys His Arg Glu
420             20
423 <210> SEQ ID NO: 14
424 <211> LENGTH: 20
425 <212> TYPE: PRT
426 <213> ORGANISM: HOMO SAPIENS
428 <400> SEQUENCE: 14
430 Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
431 1               5                  10                  15
```

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